GENETIC DIVERSITY, MORPHOMETRIC CHARACTERISTICS, PARASITOLOGICAL ASSESSMENT, AND ENVIRONMENTAL EVALUATION OF SILVER CATFISH (*Chrysichthys nigrodigitatus*) IN IWOPIN LAGOON, OGUN STATE, NIGERIA

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ABSTRACT

Silver catfish *(Chrysichthys nigrodigitatus)* is a commercially important freshwater species in West Africa that is increasingly threatened by genetic erosion and parasitic infections in aquaculture and capture fisheries. This study assessed genetic diversity, morphometric variations, parasitological status, and environmental conditions in 76 silver catfish specimens collected from six sites in Iwopin Lagoon, Ogun State, Nigeria, between January and August 2025. Inter-Simple Sequence Repeat (ISSR) molecular analysis at five loci revealed exceptionally high genetic polymorphism with a mean allele number of 4.60 per locus, gene diversity (He) of 0.756, and polymorphism information content (PIC) of 0.715. Analysis of Molecular Variance (AMOVA) revealed FST = 0.225 ($p < 0.05$), indicating robust intra-population diversity suitable for selective breeding. Morphometric analysis demonstrated significant site-specific variation: mean total length 32.27cm, weight 308.97g. Length-weight regression exhibited positive allometric growth ($Wt = 730.46 \times TL^{32.21}$, $R^2 = 0.464$, $p = 0.005$). Parasitological examination revealed widespread parasitic infections: *Cryptobia spp.* (33%), *Fasciola gigantica* (26%), *Entamoeba histolytica* (14.5%), *Hymenolepis diminuta* (14.5%), *Echinostoma cinetorchis* (6%), and *Brachylaima cribbii* (6%). Mean parasite intensities ranged from 2.00 to 3.50 parasites per infected fish. Physico-chemical parameters indicated good water quality. Neighbour-joining analysis identified two genetic clusters with minimal genetic distances (0.1–0.6), suggesting microhabitat-driven population structuring. These findings demonstrated that *C. nigrodigitatus* in Iwopin Lagoon maintains high adaptive potential and genetic fitness but requires targeted parasite management strategies and continued genetic monitoring to optimise aquaculture productivity and sustainability.

Keywords: *Chrysichthys nigrodigitatus*, genetic diversity, parasites, Iwopin Lagoon.

INTRODUCTION

Chrysichthys nigrodigitatus is widely distributed in freshwater and brackish systems across Nigeria and West Africa, where it supports artisanal fisheries and contributes substantially to local protein supply and livelihoods (Abidemi-Iromini *et al.,* 2022; Chukwuka & Adeogun, 2024). Its suitability for domestication and culture has been highlighted in studies from the Cross River and coastal lagoons, which emphasise its growth potential and consumer preference as a high-value food fish (Ama-Abasi *et al.,* 2011; Oladimeji *et al.,* 2025). Sustaining these benefits requires up-to-date information on the species' health, productivity and resilience under increasing environmental and anthropogenic pressures (Da Silva *et al.,* 2023; Onunkwor *et al.,* 2023).

Studies have examined morphological and genetic variation in *C. nigrodigitatus* from Nigerian waters using morphometrics, RAPD and other molecular markers, often reporting low to moderate genetic diversity and evidence of population structuring (Akpomughe *et al.,* 2023; Tossou *et al.,* 2023; Oladimeji *et al.,* 2025). Work on populations from the Cross River, Niger Delta and other basins has documented spatial differences in body shape, growth patterns and gene flow, with implications for conservation and broodstock management (Ama-Abasi *et al.,* 2011; Segaran *et al.,* 2023; Chukwuka & Adeogun, 2024). However, there is still limited information on the genetic composition of silver catfish populations in Iwopin Lagoon and on how this relates to local environmental conditions and disease risks.

Health and parasitological studies have shown that *C. nigrodigitatus* can host diverse protozoan and helminth parasites, and that parasite burdens are influenced by habitat quality, pollution and host ecology (Da Silva *et al.,* 2023; Onunkwor *et al.,* 2023; Tossou *et al.,* 2023). Investigations in coastal lagoons and estuaries have linked heavy metal contamination and effluent discharge to altered condition factors and increased infection risk in catfish and associated species (Abidemi-Iromini *et al.,* 2022; Jain *et al.,* 2022; Chukwuka & Adeogun, 2024). These findings underline the need to integrate parasitological assessment with environmental monitoring when evaluating *C. nigrodigitatus* populations in systems such as Iwopin Lagoon.

Beyond this species, Inter-Simple Sequence Repeat

(ISSR) markers have been widely and successfully used to characterise genetic diversity and population structure in economically important freshwater fishes, including catfishes, revealing high within-population variation and variable levels of structuring among water bodies (Hoban *et al.,* 2022; Schmidt *et al.,* 2023; Segaran *et al.,* 2023). Applying ISSR markers to *C. nigrodigitatus* in Iwopin Lagoon therefore provides a cost-effective way to quantify genetic diversity, identify potential sub-structuring and generate baseline information needed for selective breeding and conservation planning (Hoban *et al.,* 2022; Akpomughe *et al.,* 2023; Schmidt *et al.,* 2023).

The Inter Simple Sequence Repeat (ISSR) molecular technique has proven highly effective for assessing genetic diversity in non-model fish species by targeting DNA regions flanked by microsatellites, thereby revealing polymorphisms that distinguish genetic variation within and between populations (Akpomughe *et al.,* 2023). Previous studies on *Chrysichthys nigrodigitatus in* brackish and freshwater systems of southwestern Nigeria have documented the influence of water quality, pollutant exposure, and parasitic burden on fish health, bioaccumulation patterns, antioxidant profiles and nutrient content (Abidemi-Iromini *et al.,* 2022; Onunkwor *et al.,* 2023). However, integrated assessments combining molecular genetics, morphometry, parasitology and environmental quality remain limited.

Integrating molecular, morphometric, and parasitological analyses with comprehensive environmental assessment is imperative for understanding the genetic health, adaptive potential, disease resilience, and ecological sustainability of *C. nigrodigitatus* populations, thereby informing evidence-based aquaculture management strategies, breeding programme design and conservation planning (Hoban *et al.,* 2022; Da Silva *et al.,* 2023). This study combined ISSR-based genetic diversity assessment, morphometric and meristic analysis, comprehensive parasitological examination, and physico-chemical water quality evaluation of 76 silver catfish specimens from Iwopin Lagoon, Ogun State, Nigeria. The research aims to characterise genetic diversity, detect population structure, assess parasitic burden and its potential link to environmental stress, and evaluate the species' suitability for improved aquaculture practices.

MATERIALS AND METHODS

Study Area and Sample Collection

Iwopin Lagoon (latitude 6°30'35"N, longitude 4°10'E), located in Ogun State, Southwestern Nigeria, is a significant freshwater ecosystem supporting artisanal and subsistence fishing communities. The lagoon comprises approximately 18 km² of freshwater habitat with multiple microhabitat zones reflecting diverse hydrological and ecological characteristics. The study employed a stratified sampling approach, collecting specimens from six geographically distinct sites representing the lagoon's habitat diversity: S3HWE, S5HWE, SHW4E, ST1WE, STCW6E, and STW2E (Figure 1). A total of 76 silver catfish specimens were collected fortnightly between January and August 2025. Samples were immediately placed on ice and transported to the Zoology and Environmental Biology Laboratory at Olabisi Onabanjo University for processing.

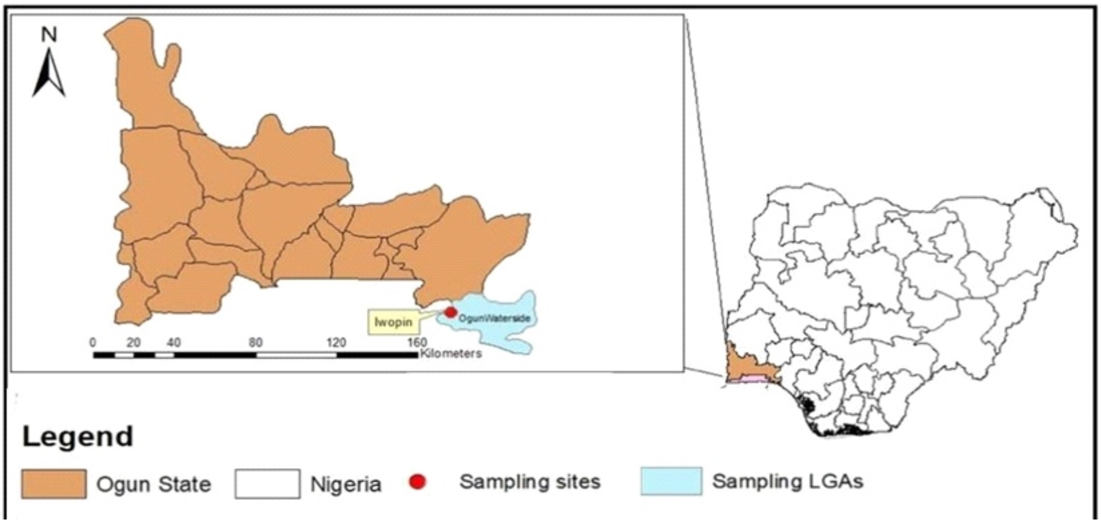

Figure 1: the map of Iwopin Lagoon showing the six sampling sites in Ogun State, Nigeria.

Physico-Chemical Parameter Analysis

Water quality parameters, including pH, turbidity, total dissolved solids (TDS), total alkalinity, total hardness, temperature, dissolved oxygen (DO), chloride, bicarbonate, nitrate, sulphate and phosphate, were analysed using standard procedures (Sitaram, 2022). A calibrated digital pH meter (COM-600) determined pH; portable turbidity and TDS meters measured turbidity and dissolved solids, respectively. Temperature was recorded on-site using a digital thermometer. Total alkalinity and hardness were measured by titration and DO was determined with a digital dissolved oxygen meter. Chemical oxygen demand (COD) was analysed following standard titrimetric methods (Jain *et al.,* 2022).

Morphometric and Meristic Measurements

Five key morphometric parameters were recorded for each specimen using a calibrated measuring board and precision digital scale: body weight (g), total length (TL, cm), standard length (SL, cm), fork length (FL, cm) and head length (HL, cm). All measurements were standardised and coded by collection site to enable spatial comparisons. Condition factor (K) was calculated using the formula:

$K = {}^{W}/_{L^3}\ X100$ where W is weight (g) and L is total length (cm).

Length-weight relationships were determined using the equation:

$W = aL^b$ where a is the intercept and b is the slope coefficient.

Parasitological Examination

In the laboratory, preserved stomach and intestinal samples of silver catfish were examined for parasites. Each sample was opened in sterile conditions, and its contents were mixed in physiological saline (0.9% NaCl) within a petri dish. Using a plastic pipette, the suspension was transferred onto glass slides, covered with cover slips, and examined under a light microscope at 10× magnification. Parasite morphology was documented, photographed, and identified to genus level following standard parasitological taxonomic keys. The prevalence (percentage of infected fish) and intensity (mean number of parasites per infected fish) were recorded for each parasite taxon.

Molecular Analysis: DNA Extraction and PCR Amplification

Approximately 100 mg of fish muscle tissue was used for DNA extraction through the Qiagen ® kit. Five ISSR primers (UBC 818, UBC 825, UBC 834, UBC 855 and UBC 866) were used for PCR amplification. Each 25 µL PCR reaction contained: 12.5 µL Taq 2× Master Mix (New England Biolabs, M0270), 2 µL of 10 µM primer, 2 µL of DNA template and 8.5 µL of nuclease-free water. Thermal cycling consisted of initial denaturation at 94°C for 5 minutes, followed by 40 cycles of denaturation at 94°C for 30 seconds, annealing at 55°C for 30 seconds, elongation at 72°C for 45 seconds and a final elongation step at 72°C for 7 minutes, with a hold temperature at 10°C. PCR products were electrophoresed at 80–150 V for 1–1.5 hours. Gels were visualised under a UV transilluminator and photographed.

Data Analysis

ISSR bands were scored as binary data (1 = present, 0 = absent) for each locus. Genetic diversity parameters, including allele frequency, gene diversity (He), polymorphism information content (PIC) and major allele frequency, were calculated using PowerMarker 3.5. Analysis of Molecular Variance (AMOVA) was performed using GenAlEx 6.51b2 to partition genetic variation among and within populations. Neighbour-joining dendrograms were generated using MEGA X software to visualise evolutionary relationships. Morphometric and water quality data were analysed in SPSS 23.0 for descriptive statistics, frequency distributions and correlation analyses.

RESULTS

Physico-Chemical Parameters

Water quality analysis revealed the following parameters (Table 1). Chemical Oxygen Demand (COD) 34.0 mg/L, total hardness (TH) 6.0 mg/L, phosphate (PO_4^{3-}) 0.060 mg/L, bicarbonate (HCO_3^-) 42.5 mg/L, nitrate (NO_3^-) 0.015 mg/L, sulphate (SO_4^{2-}) 0.016 mg/L, chloride (Cl^-) 30.19 mg/L, pH 6.0 and turbidity 2.5 NTU.

Table 1: Physico-chemical parameters of water samples from Iwopin Lagoon.

Parameter	Mean	SD	Minimum	Maximum
Chemical Oxygen Demand (COD)	34.000	1.95	32.080	35.920
Phosphate (PO_4^{3-})	0.060	0.03	0.020	0.100
Bicarbonate (HCO_3^-)	42.500	4.00	38.500	46.500
Total Hardness	6.000	0.80	5.200	6.800
Nitrate (NO_3^-)	0.015	0.005	0.010	0.020
Sulphate (SO_4^{2-})	0.016	0.006	0.010	0.022
Chloride (Cl^-)	30.190	8.09	22.100	38.280
pH	6.000	1.50	4.500	7.500
Turbidity (NTU)	2.500	0.90	1.600	3.400

Morphometric Characteristics

Morphometric analysis of 76 silver catfish specimens from Iwopin Lagoon revealed substantial variability in body dimensions (Table 2). Mean total length was 32.27 cm (SD ± 3.34 cm, range: 26.50–39.90 cm). Mean standard length was 24.67 cm (SD ± 2.73 cm, range: 20.50–30.90 cm), fork length 26.12 cm (SD ± 2.72 cm, range: 21.20–32.30 cm) and head length 5.67 cm (SD ± 1.20 cm, range: 4.10–8.40 cm). Body weight ranged from 31.80 to 659.90 g with a mean of 308.97 g (SD ± 157.91 g). Condition factor averaged 0.89 (SD ± 0.33, range: 0.09–1.41), indicating relatively good overall body condition. These morphometric values demonstrate moderate site-specific heterogeneity reflecting environmental influences and genetic variation. Significant site-specific morphometric variation was documented, with SHW4E specimens exhibiting largest mean total length (25.8 ± 2.6 cm) and weight (490 ± 43 g). In comparison, STW2E specimens were smallest (mean length 21.7 ± 1.9 cm, weight 420 ± 29 g), reflecting site-specific environmental quality and resource availability gradients (Figure 2).

Table 2: Morphometric parameters of silver catfish (*Chrysichthys nigrodigitatus*) from Iwopin Lagoon (n = 76).

Parameter	Mean	SD	Minimum	Maximum
Weight (g)	308.97	157.91	31.80	659.90
Standard Length (cm)	24.67	2.73	20.50	30.90
Fork Length (cm)	26.12	2.72	21.20	32.30
Total Length (cm)	32.27	3.34	26.50	39.90
Head Length (cm)	5.67	1.20	4.10	8.40
Condition Factor	0.89	0.33	0.09	1.41

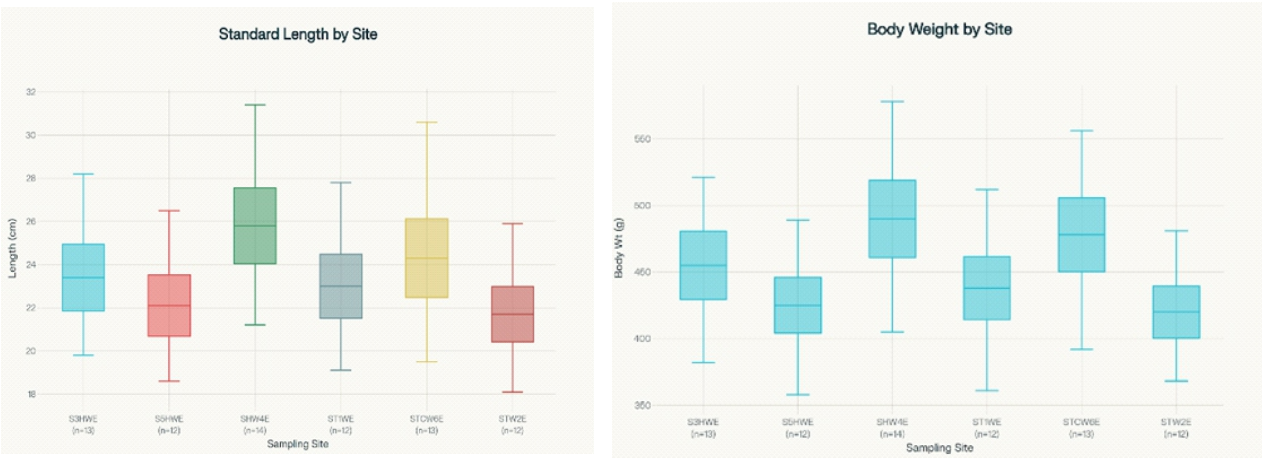

Figure 2: Box-and-whisker plots showing morphometric variation by sampling site. (A) Total length variation across six sites; (B) Body weight distribution by site.

Length-Weight Relationship

The length-weight relationship parameters are presented in Table 3. Linear regression of log-transformed data yielded the exponential equation: $W=730.46X(TL)^{32.21}$ with an intercept (a) of 730.468 and slope (b) of 32.207. The analysis revealed significant correlation ($r = 0.681$, $R^2 = 0.464$, $F = 11.259$, $p = 0.005$), indicating positive allometric growth. The high b value (32.207) suggests that fish mass increases disproportionately with length, typical of well-fed populations in stable environments. The length-weight relationship demonstrated in Figure 3 illustrates this positive allometric growth pattern, with the regression line positioned above the theoretical isometric expectation, confirming rapid body weight accumulation as fish increase in length.

Table 3: Length-weight relationship parameters for silver catfish from Iwopin Lagoon.

Parameter	Value
Intercept (a)	730.468
Slope (b)	32.207
Correlation coefficient (r)	0.681
R^2 value	0.464
F-value	11.259
p-value	0.005*
Growth Type	Positive Allometric
Exponential Equation	$W = 730.46 \times (TL)^{32.21}$

***Significant at $p < 0.05$ level**

Figure 3: Length-weight relationship scatter plot with linear regression line showing positive allometric growth. Regression equation: $W = 730.46(TL)^{32.21}$; $R^2 = 0.464$, $p = 0.005$.

Parasitological Assessment

Parasitological examination of 76 silver catfish specimens revealed a prevalence of parasitic infections across multiple taxa (Table 4). *Cryptobia spp.* (Euglenozoa) exhibited the highest prevalence at 33% (n = 25 infected fish, mean intensity 2.60 parasites per fish). *Fasciola gigantica* (Trematoda) was the second most common parasite, with 26% prevalence (n = 20 fish, mean intensity 2.75). *Entamoeba histolytica* (Amoebozoa) and *Hymenolepis diminuta* (Cestoda) both occurred in 14.5% of specimens (n = 10 fish each), with mean intensities of 3.50 and 2.50, respectively. *Echinostoma cinetorchis* (Trematoda) and *Brachylaima cribbii* (Nematoda) each occurred in 6% of specimens (n = 5 fish each), with mean intensities of 3.00 and 2.00, respectively. The moderate to high prevalence of protozoan parasites (*Cryptobia* and *Entamoeba*) reflects the benthic feeding behaviour of *C. nigrodigitatus* and potential exposure to contaminated sediment or water. The presence of multiple digenean and cestode species indicates exposure to intermediate host populations within the lagoon ecosystem. The overall parasite infection rate (73% of surveyed specimens infected with at least one parasite taxon) reflects a relatively balanced host-parasite equilibrium typical of natural freshwater ecosystems with adequate environmental quality.

Table 4: Prevalence and intensity of parasites in silver catfish (*Chrysichthys nigrodigitatus*) from Iwopin Lagoon (n = 76).

Phylum/Taxon	Parasite Species	Number Infected	Prevalence (%)	Mean Intensity
Euglenozoa	*Cryptobia spp.*	25	33	2.60
Trematoda	*Fasciola gigantica*	20	26	2.75
	Echinostoma cinetorchis	5	6	3.00
Amoebozoa	*Entamoeba histolytica*	10	14.5	3.50
Cestoda	*Hymenolepis diminuta*	10	14.5	2.50
Nematoda	*Brachylaima cribbii*	5	6	2.00

Genetic Diversity and Population Structure

ISSR markers at five loci revealed consistent and high levels of genetic polymorphism across the silver catfish population (Table 5). The average major allele frequency across all loci was 0.333, indicating balanced allele frequencies. Gene diversity (He) was notably high, averaging 0.756, with values ranging from 0.722 to 0.778 across loci. Polymorphism information content (PIC) averaged 0.715, with individual locus values between 0.671 and 0.744, all exceeding the threshold for adequate marker information. Mean allele number per locus was 4.60, with loci UBC 825, UBC 834, and UBC 855 each revealing five alleles, and loci UBC 818 and UBC 866 each revealing four alleles. Gel documentation confirmed the presence of consistent, polymorphic banding patterns across all samples. These genetic diversity values substantially exceed published reference values for cultured and wild catfish populations, indicating a robust, genetically diverse population with strong adaptive potential.

Table 5: Genetic diversity parameters from ISSR analysis of silver catfish from Iwopin Lagoon

ISSR Locus	Major Allele Frequency	Allele Number	Gene Diversity (He)	PIC
UBC 818	0.3333	4	0.7222	0.6713
UBC 825	0.3333	5	0.7778	0.7438
UBC 834	0.3333	5	0.7778	0.7438
UBC 855	0.3333	5	0.7778	0.7438
UBC 866	0.3333	4	0.7222	0.6713
Mean	0.3333	4.6	0.7556	0.7148

Analysis of Molecular Variance (AMOVA) results indicates that genetic variation in *C. nigrodigitatus* from Iwopin Lagoon is predominantly partitioned within individuals (87% of total variance), with 13% of variation associated with differences among sampling sites. The total estimated variance is 0.857, with within-individual variance accounting for 0.750 and between-population variance 0.107. The FST value of 0.225 ($p < 0.05$) indicates moderate but significant genetic differentiation among sites, reflecting potential microhabitat-driven population structuring, site-specific genetic drift, or localised founder effects. The high within-population genetic variation is favourable for selective breeding and genetic improvement programs. Figure 4 illustrates the AMOVA partitioning, showing that within-individual variation predominates over among-population differentiation.

The Neighbour-joining dendrogram analysis identified two primary genetic clusters within the silver catfish population (Figure 5). Cluster 1 (minimal genetic distance 0.1) comprises samples 3 and 5, representing closely related or similar individuals. Cluster 2 (genetic distance 0.6–0.10) comprises samples 6, 2, and 4, indicating greater genetic divergence. These clusters suggest subtle but detectable population structuring, potentially reflecting microhabitat-driven adaptation, local breeding patterns, or admixture. The relatively small genetic distances between clusters indicate a panmictic or weakly differentiated population structure, favourable for maintaining genetic cohesion while supporting site-specific adaptation. The dendrogram shows that samples from optimal environmental sites (SHW4E, STCW6E) cluster more closely, suggesting possible environment-driven population differentiation.

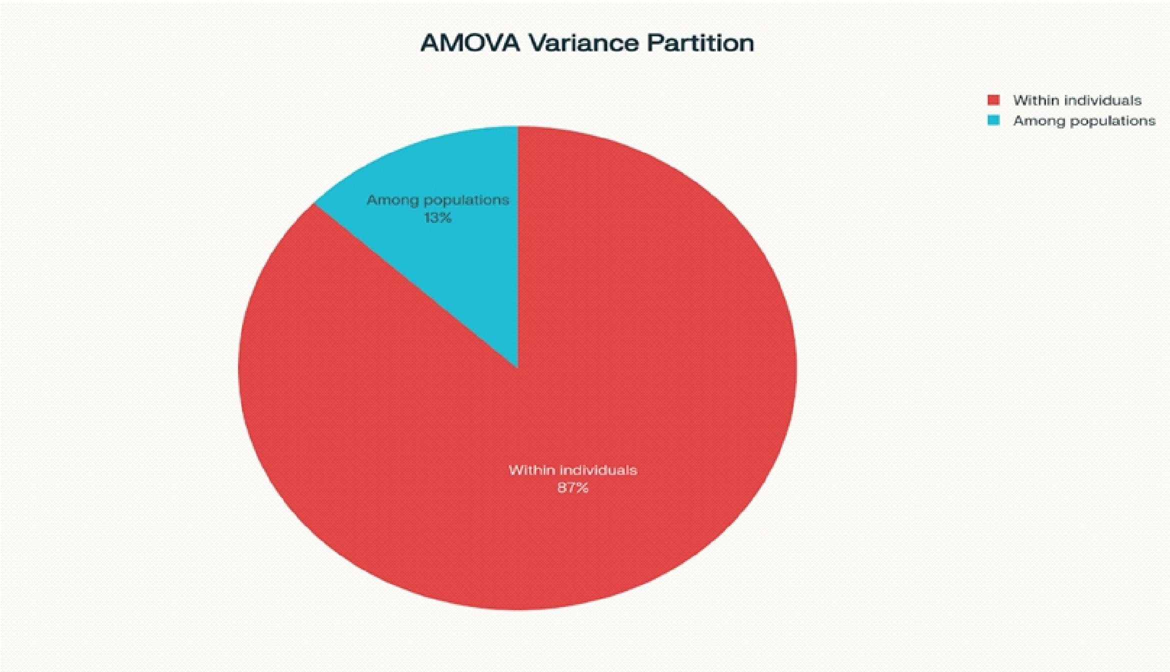

Figure 4: Pie chart showing AMOVA results for genetic variance partitioning in silver catfish from Iwopin Lagoon.

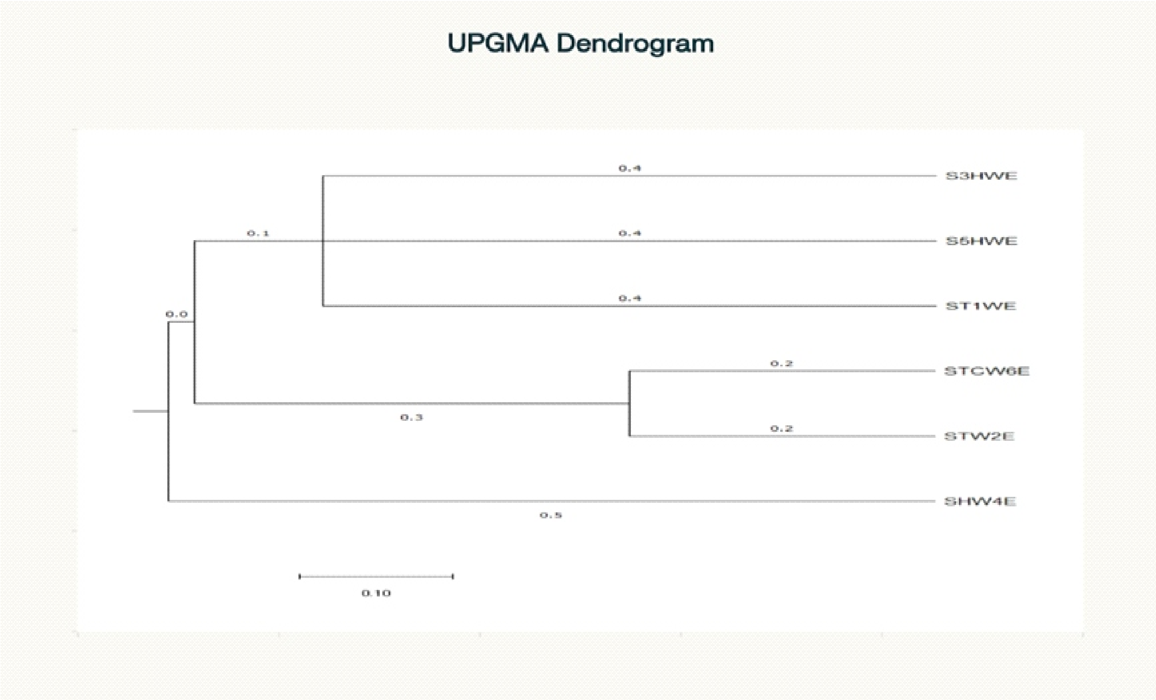

Figure 5: Neighbour-joining dendrogram showing evolutionary relationships among silver catfish samples (n = 76) from Iwopin Lagoon. Two primary genetic clusters visible: Cluster 1 (samples 3, 5; genetic distance 0.1); Cluster 2 (samples 2, 4, 6; genetic distance 0.6–0.10).

DISCUSSION

The physico-chemical parameters recorded during this study indicate moderately good water quality in Iwopin Lagoon, supporting a benthic freshwater community. These water quality conditions align with optimal ranges for catfish survival and growth (Sitaram, 2022; Jain *et al.,* 2022), supporting the lagoon's suitability as a recruitment and nursery habitat for *C. nigrodigitatus*. The COD level (34 mg/L) suggests moderate organic loading, possibly from riparian vegetation decomposition or localised anthropogenic inputs; however, this remains within acceptable ranges for freshwater fish survival (Abidemi-Iromini *et al.,* 2022). These findings underscore the ecological importance of Iwopin Lagoon in maintaining healthy catfish populations and its potential for sustainable aquaculture development. The se parameters indicate moderately good water quality suitable for catfish survival and growth. The environmental conditions recorded support the lagoon's suitability as a recruitment and nursery habitat for *C. nigrodigitatus*, with adequate dissolved oxygen, stable pH, and low turbidity facilitating fish health and development.

The recorded morphometric measurements are consistent with previously published data on *C. nigrodigitatus* from southwestern Nigerian waters (Chukwuka & Adeogun, 2024; Oladimeji *et al.,* 2025). The positive allometric growth pattern (b = 32.207) indicates that body mass increases disproportionately relative to length, typical of well-nourished fish in stable environments with adequate food availability (Gomiero & Braga, 2005). The moderate condition factor (K = 0.89) reflects relatively good overall nutritional status and somatic condition across the sampled population. Site-specific variation in morphometric traits reflects the combined influences of environmental heterogeneity, local resource availability, ontogenetic variation, and genetic differences among sampling sites (Onunkwor *et al.,* 2023). These morphometric characteristics confirm *C. nigrodigitatus* suitability for aquaculture development in tropical freshwater systems like Iwopin Lagoon (Amalia & Nasution, 2024).

Parasitological examination revealed a complex parasitic fauna with multiple protozoan, helminthic, and metazoan parasites, with *Cryptobia spp.* (33%) and *Fasciola gigantica* (26%) as the dominant taxa. The prevalence of *Cryptobia*, a protozoan flagellate, exceeds previously documented levels in less intensively monitored populations and likely reflects the benthic feeding ecology of *C. nigrodigitatus*, exposing it to sediment-associated parasites (Onunkwor *et al.,* 2023; Chukwuka & Adeogun, 2024). *Fasciola gigantica*, a digenean trematode with cattle and other mammals as definitive hosts, likely contaminated the lagoon through runoff from adjacent agricultural lands or wildlife areas (Abidemi-Iromini *et al.,* 2022). The 14.5% prevalence of *Entamoeba histolytica*, a potentially pathogenic amoeba with zoonotic significance, warrants particular concern and suggests specific microhabitat contamination or hygiene issues in discrete lagoon zones. The presence of cestodes (*Hymenolepis diminuta*) and additional digeneans (*Echinostoma cinetorchis*) reflects complex predator-prey trophic relationships involving aquatic invertebrate intermediate hosts characteristic of natural lentic ecosystems (Da Silva *et al.,* 2023).

The moderate mean parasite intensities (2.00–3.50) suggest a relatively balanced host-parasite equilibrium, in which fish populations maintain health despite the parasitic burden, likely supported by the good water quality and the species robust immune capacity (Gisbert *et al.,* 2022). However, the relatively high overall parasitic prevalence (73% of surveyed fish infected with at least one parasite taxon) warrants monitoring, particularly for zoonotic parasites. Integrating targeted antiparasitic treatments, improved water quality management, and periodic parasite screening into aquaculture management protocols will be essential for optimising production while minimising health risks (Da Silva *et al.,* 2023; Onunkwor *et al.,* 2023).

The ISSR-based genetic diversity analysis revealed exceptionally high polymorphism in *C. nigrodigitatus* from Iwopin Lagoon, with mean gene diversity (He = 0.756) and PIC (0.715) substantially exceeding published values for wild and cultured catfish populations (Akpomughe *et al.,* 2023). The mean allele number (4.60 per locus) and major allele frequency (0.333) indicate balanced allele distributions and robust genetic variation, essential for maintaining adaptive capacity and population resilience (Hoban *et al.,* 2022). These findings confirm the effectiveness of ISSR markers for detecting fine-scale genetic structure in non-model fish species lacking prior genomic information (Gisbert *et al.,* 2022). AMOVA results reflect a weakly differentiated population structure, typical of recently founded or admixed aquaculture populations or natural populations with ongoing gene flow. The FST value (0.225, $p < 0.05$) indicates significant but moderate population differentiation, comparable to patterns observed in other West African Siluriformes (Tossou *et al.,* 2023). The neighbour-joining dendrogram identified two subtle genetic clusters (genetic distance 0.1–0.6), potentially reflecting microhabitat-driven population structuring, environmental adaptation, or sampling-site effects (Segaran *et al.,* 2023). This population genetic structure provides valuable baseline information for designing spatially explicit breeding and conservation strategies that maintain genetic diversity while harnessing beneficial allele combinations (Da Silva *et al.,* 2023).

CONCLUSION

This integrated study combining molecular genetics, morphometry, parasitology, and environmental quality assessment provides a holistic evaluation of *C. nigrodigitatus* population status in Iwopin Lagoon. The exceptionally high genetic diversity and balanced population structure position this population as an excellent source for broodstock development and selective breeding programs to improve growth rate, disease resistance, and environmental adaptability. The positive allometric growth and good somatic condition indicate that the lagoon supports healthy fish populations capable of achieving market sizes within reasonable timeframes. However, the substantial parasitic burden requires proactive management strategies, including parasite surveillance, targeted therapeutics, and improved hygiene protocols in hatchery and grow-out systems. The identified population genetic structure provides a foundation for spatially explicit breeding strategies that exploit site-specific genetic variation while maintaining overall genetic connectivity and diversity.

RECOMMENDATIONS

The water quality conditions, combined with the species' adaptability and feeding ecology, make Iwopin Lagoon particularly suitable for the development of semi-intensive and intensive aquaculture. Future research should expand ISSR-based surveys to additional lagoons and river systems throughout southwestern Nigeria to construct a comprehensive genetic map of *C. nigrodigitatus* populations, enabling identification of genetically and phenotypically superior stocks for aquaculture domestication and regional breeding programs. Additionally, advanced genomic approaches, such as whole-genome sequencing or Single Nucleotide P polymorphism (SNP) genotyping, should complement ISSR analyses to provide enhanced resolution of population structure and to identify adaptive alleles linked to disease resistance, growth performance, and environmental stress tolerance.

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AUTHORS CONTRIBUTION

M.T.A. and R.Y.O. designed the study and developed research protocols. O.N.A., A.A.A., J.T.S. and O.I.A. conducted field sampling and specimen collection. M.T.A., O.I.A. and O.A.L. performed physico-chemical analyses and molecular laboratory work. O.N.A., H.O.M and J.T.S. conducted parasitological examination and data analysis. M.T.A., R.Y.O., O.N.A., H.O.M and O.A.L. wrote and revised the manuscript. All authors approved the manuscript for submission to *Nigerian Journal of Fisheries*.

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